

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/518,223  
Source: IFW/b  
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IFW16

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/518,223

DATE: 06/23/2006  
TIME: 13:06:07

Input Set : A:\EAGIP5.001APC.TXT  
Output Set: N:\CRF4\06232006\J518223.raw

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4 <110> APPLICANT: Cheng, Ning Man
5     Leung, Yun Chung
6     Lo, Wai Hung
8 <120> TITLE OF INVENTION: PHARMACEUTICAL PREPARATION AND METHOD OF
9     TREATMENT OF HUMAN MALIGNANCIES WITH ARGININE DEPRIVATION
12 <130> FILE REFERENCE: EAGIP5.001APC
14 <140> CURRENT APPLICATION NUMBER: 10/518,223
15 <141> CURRENT FILING DATE: 2004-12-15
17 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/002665
18 <151> PRIOR FILING DATE: 2003-06-20
20 <150> PRIOR APPLICATION NUMBER: PCT/CN02/00635
21 <151> PRIOR FILING DATE: 2002-09-09
23 <150> PRIOR APPLICATION NUMBER: 60/390,757
24 <151> PRIOR FILING DATE: 2002-06-20
26 <160> NUMBER OF SEQ ID NOS: 9
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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31 <211> LENGTH: 2002
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
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37 aagtgaaatg cgaggaaatg ccaagaaaatg gtgattatga ggggtgttat ttcacaaaaa 120
38 acggagaata tttattggaa ttaagagtct ctgggactgc tcttgtaat gtccttgtta 180
39 atttaaagga tattgacata acgaaatggt tgtgtaaaac agggagatta tatcttgata 240
40 aggttaagaa atttgaaaata gttactattc tttcccatgta cgtagaaaat caaaagatta 300
41 taacagaatg ggagtcaactc cccagagagg ctttacccga acaatttgat tcataagaac 360
42 taatttagtag cgctttccaa tgaggcgct ttttatttg ggtagttgca taccactaaa 420
43 gatgttcagg tgcacatgag cattggagga aaggaacgct ttagggggaa gggaaacctt 480
44 taaacagtct taatccccct tgattttatg ttctctgtaa actgcgtccg gtaaatctca 540
45 ggatagacaa tcggcggtta acggcttgag tgcggggca gtttagaaag aatatgattg 600
46 gagggattca tagatgcattc accatcacca tcatatgagc gccaagtcca gaaccatagg 660
47 gattatttggaa gtcctttct caaagggaca gccacggagga ggggtggaaag aaggccctac 720
48 agtattgaga aaggctggtc tgcttgagaa acttaaagaa caagagtgtg atgtgaagga 780
49 ttatgggac ctgcccttgc ctgacatccc taatgacagt cccttcaaa ttgtgaagaa 840
50 tccaaagggtct gtggggaaaag caagcgagca gctggctggc aagggtggcac aagtcaagaa 900
51 gaacggaaga atcagctgg tgcgtggcgg agaccacagt ttggcaatttga gaagcatctc 960
52 tggccatgcc agggtccacc ctgatcttgg agtcatctgg gtggatgctc acactgatat 1020
53 caacactcca ctgacaacca caagtggaaa cttgcatttgc caacctgtat ctttccctc 1080
54 gaaggaacta aaaggaaaaga ttcccgatgt gccaggattc tcctgggtga ctccctgtat 1140
55 atctgccaag gatattgtgt atattggctt gagagacgtg gaccctgggg aacactacat 1200
56 ttgaaaact ctaggcatta aatactttc aatgactgaa gtggacagac taggaatttgg 1260
57 caaggtgatg gaagaaacac tcagctatct actagaaga aagaaaaggc caattcatct 1320

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58 aagtttgat gttgacggac tggacccatc tttcacacca gctactggca caccagtcgt 1380  
 59 gggaggctcg acatacagag aaggtctcta catcacagaa gaaatctaca aaacaggcgt 1440  
 60 actctcagga tttagatataa tggaaagtgaa cccatccctg ggaaagacac cagaagaagt 1500  
 61 aactcgaaca gtgaacacag cagttgcaat aaccttggct tgtttggac ttgctcggga 1560  
 62 gggtaatcac aagcctattg actaccttaa cccacctaag taaatgtgga aacatccgt 1620  
 63 ataaatctca tagttaatgg cataattaga aagctaatca ttttcttaag catagagtt 1680  
 64 tccttctaaa gacttgttct ttcagaaaaa tgttttcca attagtataa actctacaaa 1740  
 65 ttccctcttg gtgtaaaatt caagatgtgg aaattctaac tttttgaaa tttaaaagct 1800  
 66 tatattttct aacttggcaa aagacttac cttagaaaga gaagtgtaca ttgatttcca 1860  
 67 attaaaaatt tgctggcatt aaaaataaagc acacttacat aagccccat acatagagtg 1920  
 68 ggactcttgg aatcaggaga caaagctacc acatgtggaa aggtactatg tgtccatgtc 1980  
 69 attcaaaaaa tgtgattcta ga 2002

71 <210> SEQ ID NO: 2  
 72 <211> LENGTH: 990  
 73 <212> TYPE: DNA  
 74 <213> ORGANISM: Artificial Sequence  
 76 <220> FEATURE:  
 77 <223> OTHER INFORMATION: Chimeric DNA sequence encoding human arginase I  
 78 and an N-terminal histidine tag  
 80 <400> SEQUENCE: 2

81 atg cat cac cat cac cat atg agc gcc aag tcc aga acc ata ggg 48  
 82 att att gga gct cct ttc tca aag gga cag cca cga gga ggg gtg gaa 96  
 83 gaa ggc cct aca gta ttg aga aag gct ggt ctg ctt gag aaa ctt aaa 144  
 84 gaa caa gag tgt gat gtg aag gat tat ggg gac ctg ccc ttt gct gac 192  
 85 atc cct aat gac agt ccc ttt caa att gtg aag aat cca agg tct gtg 240  
 86 gga aaa gca agc gag cag ctg gct ggc aag gtg gca caa gtc aag aag 288  
 87 aac gga aga atc agc ctg gtg ctg ggc gga gac cac agt ttg gca att 336  
 88 gga agc atc tct ggc cat gcc agg gtc cac cct gat ctt gga gtc atc 384  
 89 tgg gtg gat gct cac act gat atc aac act cca ctg aca acc aca agt 432  
 90 gga aac ttg cat gga caa cct gta tct ttc ctc ctg aag gaa cta aaa 480  
 91 gga aag att ccc gat gtg cca gga ttc tcc tgg gtg act ccc tgt ata 528  
 92 tct gcc aag gat att gtg tat att ggc ttg aga gac gtg gac cct ggg 576  
 93 gaa cac tac att ttg aaa act cta ggc att aaa tac ttt tca atg act 624  
 94 gaa gtg gac aga cta gga att ggc aag gtg atg gaa gaa aca ctc agc 672  
 95 tat cta cta gga aga aag aaa agg cca att cat cta agt ttt gat gtt 720  
 96 gac gga ctg gac cca tct ttc aca cca gct act ggc aca cca gtc gtg 768  
 97 gga ggt ctg aca tac aga gaa ggt ctc tac atc aca gaa gaa atc tac 816  
 98 aaa aca ggg cta ctc tca gga tta gat ata atg gaa gtg aac cca tcc 864  
 99 ctg ggg aag aca cca gaa gta act cga aca gtg aac aca gca gtt 912  
 100 gca ata acc ttg gct tgt ttc gga ctt gct cgg gag ggt aat cac aag 960  
 101 cct att gac tac ctt aac cca cct aag taa 990

103 <210> SEQ ID NO: 3  
 104 <211> LENGTH: 329  
 105 <212> TYPE: PRT  
 106 <213> ORGANISM: Artificial Sequence  
 108 <220> FEATURE:  
 109 <223> OTHER INFORMATION: Chimeric AA sequence of human arginase I and an  
 110 N-terminal histidine tag  
 112 <400> SEQUENCE: 3

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113 Met His His His His His Met Ser Ala Lys Ser Arg Thr Ile Gly
114   1           5           10          15
115 Ile Ile Gly Ala Pro Phe Ser Lys Gly Gln Pro Arg Gly Gly Val Glu
116   20          25          30
117 Glu Gly Pro Thr Val Leu Arg Lys Ala Gly Leu Leu Glu Lys Leu Lys
118   35          40          45
119 Glu Gln Glu Cys Asp Val Lys Asp Tyr Gly Asp Leu Pro Phe Ala Asp
120   50          55          60
121 Ile Pro Asn Asp Ser Pro Phe Gln Ile Val Lys Asn Pro Arg Ser Val
122   65          70          75          80
123 Gly Lys Ala Ser Glu Gln Leu Ala Gly Lys Val Ala Gln Val Lys Lys
124   85          90          95
125 Asn Gly Arg Ile Ser Leu Val Leu Gly Gly Asp His Ser Leu Ala Ile
126   100         105         110
127 Gly Ser Ile Ser Gly His Ala Arg Val His Pro Asp Leu Gly Val Ile
128   115         120         125
129 Trp Val Asp Ala His Thr Asp Ile Asn Thr Pro Leu Thr Thr Thr Ser
130   130         135         140
131 Gly Asn Leu His Gly Gln Pro Val Ser Phe Leu Leu Lys Glu Leu Lys
132   145         150         155         160
133 Gly Lys Ile Pro Asp Val Pro Gly Phe Ser Trp Val Thr Pro Cys Ile
134   165         170         175
135 Ser Ala Lys Asp Ile Val Tyr Ile Gly Leu Arg Asp Val Asp Pro Gly
136   180         185         190
137 Glu His Tyr Ile Leu Lys Thr Leu Gly Ile Lys Tyr Phe Ser Met Thr
138   195         200         205
139 Glu Val Asp Arg Leu Gly Ile Gly Lys Val Met Glu Glu Thr Leu Ser
140   210         215         220
141 Tyr Leu Leu Gly Arg Lys Lys Arg Pro Ile His Leu Ser Phe Asp Val
142   225         230         235         240
143 Asp Gly Leu Asp Pro Ser Phe Thr Pro Ala Thr Gly Thr Pro Val Val
144   245         250         255
145 Gly Gly Leu Thr Tyr Arg Glu Gly Leu Tyr Ile Thr Glu Glu Ile Tyr
146   260         265         270
147 Lys Thr Gly Leu Leu Ser Gly Leu Asp Ile Met Glu Val Asn Pro Ser
148   275         280         285
149 Leu Gly Lys Thr Pro Glu Glu Val Thr Arg Thr Val Asn Thr Ala Val
150   290         295         300
151 Ala Ile Thr Leu Ala Cys Phe Gly Leu Ala Arg Glu Gly Asn His Lys
152   305         310         315         320
153 Pro Ile Asp Tyr Leu Asn Pro Pro Lys
154   325
157 <210> SEQ ID NO: 4
158 <211> LENGTH: 7
159 <212> TYPE: PRT
160 <213> ORGANISM: Artificial Sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: 6x Histidine tag
165 <400> SEQUENCE: .4

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 Output Set: N:\CRF4\06232006\J518223.raw

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166 Met His His His His His
167   1           5
170 <210> SEQ ID NO: 5
171 <211> LENGTH: 33
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence
178 <400> SEQUENCE: 5
179 ccaaaccata tgagcgccaa gtccagaacc ata          33
181 <210> SEQ ID NO: 6
182 <211> LENGTH: 39
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence
189 <400> SEQUENCE: 6
190 ccaaactcta gaatcacatt ttttgaatga catggacac          39
192 <210> SEQ ID NO: 7
193 <211> LENGTH: 24
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Synthetic oligonucleotide primer sequence
200 <400> SEQUENCE: 7
201 ctctggccat gccagggtcc accc          24
203 <210> SEQ ID NO: 8
204 <211> LENGTH: 969
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (1)...(969)
212 <400> SEQUENCE: 8
213 atg agc gcc aag tcc aga acc ata ggg att att gga gct cct ttc tca    48
214 Met Ser Ala Lys Ser Arg Thr Ile Gly Ile Ile Gly Ala Pro Phe Ser
215   1           5           10           15
217 aag gga cag cca cga gga ggg gtg gaa gaa ggc cct aca gta ttg aga          96
218 Lys Gly Gln Pro Arg Gly Gly Val Glu Glu Gly Pro Thr Val Leu Arg
219   20           25           30
221 aag gct ggt ctg ctt gag aaa ctt aaa gaa caa gag tgt gat gtg aag          144
222 Lys Ala Gly Leu Leu Glu Lys Leu Lys Glu Gln Glu Cys Asp Val Lys
223   35           40           45
225 gat tat ggg gac ctg ccc ttt gct gac atc cct aat gac agt ccc ttt          192
226 Asp Tyr Gly Asp Leu Pro Phe Ala Asp Ile Pro Asn Asp Ser Pro Phe
227   50           55           60
229 caa att gtg aag aat cca agg tct gtg gga aaa gca agc gag cag ctg          240
230 Gln Ile Val Lys Asn Pro Arg Ser Val Gly Lys Ala Ser Glu Gln Leu
231   65           70           75           80

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233	gct	ggc	aag	gtg	gca	caa	gtc	aag	aac	gga	aga	atc	agc	ctg	gtg	288	
234	Ala	Gly	Lys	Val	Ala	Gln	Val	Lys	Lys	Asn	Gly	Arg	Ile	Ser	Leu	Val	
235																95	
237	ctg	ggc	gga	gac	cac	agt	ttg	gca	att	gga	agc	atc	tct	ggc	cat	gcc	336
238	Leu	Gly	Gly	Asp	His	Ser	Leu	Ala	Ile	Gly	Ser	Ile	Ser	Gly	His	Ala	
239																110	
241	agg	gtc	cac	cct	gat	ctt	gga	gtc	atc	tgg	gtg	gat	gct	cac	act	gat	384
242	Arg	Val	His	Pro	Asp	Leu	Gly	Val	Ile	Trp	Val	Asp	Ala	His	Thr	Asp	
243																125	
245	atc	aac	act	cca	ctg	aca	acc	aca	agt	gga	aac	ttg	cat	gga	caa	cct	432
246	Ile	Asn	Thr	Pro	Leu	Thr	Thr	Thr	Ser	Gly	Asn	Ieu	His	Gly	Gln	Pro	
247																140	
249	gta	tct	ttc	ctc	ctg	aag	gaa	cta	aaa	gga	aag	att	ccc	gat	gtg	cca	480
250	Val	Ser	Phe	Leu	Leu	Lys	Glu	Leu	Lys	Gly	Lys	Ile	Pro	Asp	Val	Pro	
251	145															160	
253	gga	ttc	tcc	tgg	gtg	act	ccc	tgt	ata	tct	gcc	aag	gat	att	gtg	tat	528
254	Gly	Phe	Ser	Trp	Val	Thr	Pro	Cys	Ile	Ser	Ala	Lys	Asp	Ile	Val	Tyr	
255																175	
257	att	ggc	ttg	aga	gac	gtg	gac	cct	ggg	gaa	cac	tac	att	ttg	aaa	act	576
258	Ile	Gly	Leu	Arg	Asp	Val	Asp	Pro	Gly	Glu	His	Tyr	Ile	Leu	Lys	Thr	
259																190	
261	cta	ggc	att	aaa	tac	ttt	tca	atg	act	gaa	gtg	gac	aga	cta	gga	att	624
262	Leu	Gly	Ile	Lys	Tyr	Phe	Ser	Met	Thr	Glu	Val	Asp	Arg	Leu	Gly	Ile	
263																205	
265	ggc	aag	gtg	atg	gaa	gaa	aca	ctc	agt	tat	cta	gga	aga	aag	aaa	672	
266	Gly	Lys	Val	Met	Glu	Glu	Thr	Leu	Ser	Tyr	Leu	Gly	Arg	Lys	Lys		
267																220	
269	agg	cca	att	cat	cta	agt	ttt	gat	gtt	gac	gga	ctg	gac	cca	tct	ttc	720
270	Arg	Pro	Ile	His	Leu	Ser	Phe	Asp	Val	Asp	Gly	Leu	Asp	Pro	Ser	Phe	
271	225															240	
273	aca	cca	gct	act	ggc	aca	cca	gtc	gtg	gga	ggt	ctg	aca	tac	aga	gaa	768
274	Thr	Pro	Ala	Thr	Gly	Thr	Pro	Val	Val	Gly	Gly	Leu	Thr	Tyr	Arg	Glu	
275																255	
277	ggt	ctc	tac	atc	aca	gaa	gaa	atc	tac	aaa	aca	ggg	cta	ctc	tca	gga	816
278	Gly	Leu	Tyr	Ile	Thr	Glu	Glu	Ile	Tyr	Lys	Thr	Gly	Leu	Leu	Ser	Gly	
279																270	
281	tta	gat	ata	atg	gaa	gtg	aac	cca	tcc	ctg	ggg	aag	aca	cca	gaa	gaa	864
282	Leu	Asp	Ile	Met	Glu	Val	Asn	Pro	Ser	Leu	Gly	Lys	Thr	Pro	Glu	Glu	
283																285	
285	gta	act	cga	aca	gtg	aac	aca	gca	gtt	gca	ata	acc	ttg	gct	tgt	ttc	912
286	Val	Thr	Arg	Thr	Val	Asn	Thr	Ala	Val	Ala	Ile	Thr	Leu	Ala	Cys	Phe	
287																300	
289	gga	ctt	gct	cgg	gag	ggt	aat	cac	aag	cct	att	gac	tac	ctt	aac	cca	960
290	Gly	Leu	Ala	Arg	Glu	Gly	Asn	His	Lys	Pro	Ile	Asp	Tyr	Leu	Asn	Pro	
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294	Pro	Lys	*														
298	<210>	SEQ ID NO:	9														
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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/518,223

DATE: 06/23/2006

TIME: 13:06:08

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